

0400 04-18-01

#2 OIPE

RAW SEQUENCE LISTING

DATE: 04/05/2001

PATENT APPLICATION: US/09/813,329

TIME: 12:43:12

Input Set : A:\PTO.txt

Output Set: N:\CRF3\04052001\I813329.raw

ENTERED

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3 <110> APPLICANT: Bristol-Myers Suibb Company
5 <120> TITLE OF INVENTION: Novel Drosophila Tumor Necrosis Factor Class Molecule ("DmTNF") and
6   Variants Thereof
8 <130> FILE REFERENCE: D0016.np
C--> 10 <140> CURRENT APPLICATION NUMBER: US/09/813,329
C--> 10 <141> CURRENT FILING DATE: 2001-03-20
10 <150> PRIOR APPLICATION NUMBER: 60/190,816
11 <151> PRIOR FILING DATE: 2000-03-21
13 <160> NUMBER OF SEQ ID NOS: 65
15 <170> SOFTWARE: PatentIn version 3.0
17 <210> SEQ ID NO: 1
18 <211> LENGTH: 2166
19 <212> TYPE: DNA
20 <213> ORGANISM: Drosophila melanogaster
22 <220> FEATURE:
23 <221> NAME/KEY: CDS
24 <222> LOCATION: (652)..(1878)
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29 taaatcagag atcccaagca agcgcgtgcg tgcatgatag cgaagaaaaa aagctatccg      120
31 tttcagttaa ctacttacca agattgaatt tcgccatcgg gcaaattact aaaaatacat      180
33 aagtgcgaact cgtccactgt gtgtgtgtgtt tttttttttt tttttggttt tcgctgtgcc      240
35 tttatcgcaa acaagaactg ataaaaactag aaaaatatctt gagaaacttg ttttcgcgct      300
37 tttcttttgc taattgccga tcgcggaaga gaaaaacaag cagtagacaa aacaagtgtg      360
39 gtaatacaat ctgaaaaggg caccatcagc agcccgaggg gtttatctat atagatgtcg      420
41 cagcttatca tctcatgctg tctgtgaggt tgttctgtgt gctcgtgtag tatcttaaat      480
43 acatagagtg tgttcatata aagtgcgaca aagctcgatt ggaaacagct gtcgagtgcc      540
45 cttgagtggg tgggcaagat cgtcatcatc atcatcgtcg tcattatcaa cagaatcagc      600
47 atcagcatct ggaggccccg gatgctctaa gatccccagt gttcatcaat t atg act      657
48                                     Met Thr
49                                     1
51 gcc gag acc ctc aag ccg ttt ata acg cca acg agt gcc aac gat gat      705
52 Ala Glu Thr Leu Lys Pro Phe Ile Thr Pro Thr Ser Ala Asn Asp Asp
53      5              10              15
55 ggt ttt ccg gcc aaa gcg acc agc acg gcg acc gcc cag cga cgc acc      753
56 Gly Phe Pro Ala Lys Ala Thr Ser Thr Ala Thr Ala Gln Arg Arg Thr
57      20              25              30
59 cgc cag ctg atc ccc ctg gtt ttg ggg ttc atc ggt ctg ggg ctg gtc      801
60 Arg Gln Leu Ile Pro Leu Val Leu Gly Phe Ile Gly Leu Gly Leu Val
61 35              40              45              50
63 gtt gcc att ctc gca cta acg atc tgg cag aca acg cgt gta tcg cat      849
64 Val Ala Ile Leu Ala Leu Thr Ile Trp Gln Thr Thr Arg Val Ser His
65      55              60              65
67 ctg gac aag gag ctg aag agc ctg aag cga gtc gtc gat aat ctc cag      897
68 Leu Asp Lys Glu Leu Lys Ser Leu Lys Arg Val Val Asp Asn Leu Gln
69      70              75              80
71 cag cgt ttg ggc ata aac tat ctg gac gag ttc gac gag ttc caa aag      945

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72 Gln Arg Leu Gly Ile Asn Tyr Leu Asp Glu Phe Asp Glu Phe Gln Lys
73      85      90      95
75 gag tac gag aat gcc ctc atc gac tat cca aaa aag gtg gat ggc ctc      993
76 Glu Tyr Glu Asn Ala Leu Ile Asp Tyr Pro Lys Lys Val Asp Gly Leu
77      100      105      110
79 acg gat gag gag gac gac gac gat ggc gat ggt ctg gat tcc att gcg      1041
80 Thr Asp Glu Glu Asp Asp Asp Asp Gly Asp Gly Leu Asp Ser Ile Ala
81      115      120      125      130
83 gac gac gag gac gac gac gtt agc tat agc tct gtg gat gat gtt ggc      1089
84 Asp Asp Glu Asp Asp Val Ser Tyr Ser Ser Val Asp Asp Val Gly
85      135      140      145
87 gca gac tac gag gac tac acc gat atg tta aat aaa ctc aac aat gca      1137
88 Ala Asp Tyr Glu Asp Tyr Thr Asp Met Leu Asn Lys Leu Asn Asn Ala
89      150      155      160
91 cat acc ggc acc acg ccc aca tct gag acc act gct gag ggc gag ggc      1185
92 His Thr Gly Thr Thr Pro Thr Ser Glu Thr Thr Ala Glu Gly Glu Gly
93      165      170      175
95 gag acg gac agt gca tcc tca gcc tca aat gat gac aat gtg ttc gat      1233
96 Glu Thr Asp Ser Ala Ser Ser Ala Ser Asn Asp Asp Asn Val Phe Asp
97      180      185      190
99 gac ttt acc agc tca gat gcc ctc aaa aag aag cag gag aga aaa tct      1281
100 Asp Phe Thr Ser Ser Asp Ala Leu Lys Lys Lys Gln Glu Arg Lys Ser
101      195      200      205      210
103 cgc tcg att gcc gat gta cgc aat gag gag cag aat att caa gga aat      1329
104 Arg Ser Ile Ala Asp Val Arg Asn Glu Glu Gln Asn Ile Gln Gly Asn
105      215      220      225
107 cac aca gag ctt cag gaa aag tca tcc aat gag gca gct tcc aaa gag      1377
108 His Thr Glu Leu Gln Glu Lys Ser Ser Asn Glu Ala Ala Ser Lys Glu
109      230      235      240
111 agc cct gca gca ctt cac ctc cgt cgc aga atg cat tcc cgc cat cgc      1425
112 Ser Pro Ala Ala Leu His Leu Arg Arg Arg Met His Ser Arg His Arg
113      245      250      255
115 cac ctc gta gtc cgc aaa gcc aga tcc gag gac tcg agg cca gca gcc      1473
116 His Leu Val Val Arg Lys Ala Arg Ser Glu Asp Ser Arg Pro Ala Ala
117      260      265      270
119 cat ttc cac ttg agc agc agg cgg cgt cac caa gaa agt atg ggc tac      1521
120 His Phe His Leu Ser Ser Arg Arg Arg His Gln Glu Ser Met Gly Tyr
121      275      280      285      290
123 cat gga gat atg tac ata gaa aat gat agg gag aga tgc tct tat cag      1569
124 His Gly Asp Met Tyr Ile Glu Asn Asp Arg Glu Arg Cys Ser Tyr Gln
125      295      300      305
127 gga cac ttt caa acg cgc gat ggc gta ttg acg gtg acc aat gca ggc      1617
128 Gly His Phe Gln Thr Arg Asp Gly Val Leu Thr Val Thr Asn Ala Gly
129      310      315      320
131 cta tat tac gta tac gcc cag ata tgg ggc tac aac tcg cac gac cag      1665
132 Leu Tyr Tyr Val Tyr Ala Gln Ile Trp Gly Tyr Asn Ser His Asp Gln
133      325      330      335
135 aac gga ttt atc gtc ttt caa gga gac act cca ttc ctg cag tgc ttg      1713
136 Asn Gly Phe Ile Val Phe Gln Gly Asp Thr Pro Phe Leu Gln Cys Leu

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137      340      345      350
139 aac acg gtg ccc acc aac atg cca cat aag gtg cac acc tgc cac acg      1761
140 Asn Thr Val Pro Thr Asn Met Pro His Lys Val His Thr Cys His Thr
141 355      360      365      370
143 agt ggt ctg atc cac ctg gaa cga aac gag agg atc cat ctg aag gac      1809
144 Ser Gly Leu Ile His Leu Glu Arg Asn Glu Arg Ile His Leu Lys Asp
145      375      380      385
147 att cac aac gat cgc aat gca gtt ctg cgg gag gga aac aac cga agc      1857
148 Ile His Asn Asp Arg Asn Ala Val Leu Arg Glu Gly Asn Asn Arg Ser
149      390      395      400
151 tac ttt ggc atc ttc aag gtg taaattggag agattatccc cggtcagaag      1908
152 Tyr Phe Gly Ile Phe Lys Val
153      405
155 atggaataacc agttaaagct tttgtcccccg cgactgctcg tgaatgcgat tcatcgccag      1968
157 cgtgaatcca ttagttcgta gtacctagtc ttagtcactc caaacctaata ctcaatcgga      2028
159 atcgtgcata ctgcattagt cagaagacgg aggaaaatca tatttatttt gtatatatac      2088
161 gttcgactct aaaaagtga taaaaatata tgtagctatt aaaaaaaaaa aaaaaaaaaa      2148
163 aaaaaaaaaa acctcgag      2166
166 <210> SEQ ID NO: 2
167 <211> LENGTH: 409
168 <212> TYPE: PRT
169 <213> ORGANISM: Drosophila melanogaster
171 <400> SEQUENCE: 2
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174 1      5      10      15
177 Asp Asp Gly Phe Pro Ala Lys Ala Thr Ser Thr Ala Thr Ala Gln Arg
178      20      25      30
181 Arg Thr Arg Gln Leu Ile Pro Leu Val Leu Gly Phe Ile Gly Leu Gly
182      35      40      45
185 Leu Val Val Ala Ile Leu Ala Leu Thr Ile Trp Gln Thr Thr Arg Val
186      50      55      60
189 Ser His Leu Asp Lys Glu Leu Lys Ser Leu Lys Arg Val Val Asp Asn
190 65      70      75      80
193 Leu Gln Gln Arg Leu Gly Ile Asn Tyr Leu Asp Glu Phe Asp Glu Phe
194      85      90      95
197 Gln Lys Glu Tyr Glu Asn Ala Leu Ile Asp Tyr Pro Lys Lys Val Asp
198      100      105      110
201 Gly Leu Thr Asp Glu Glu Asp Asp Asp Asp Gly Asp Gly Leu Asp Ser
202      115      120      125
205 Ile Ala Asp Asp Glu Asp Asp Asp Val Ser Tyr Ser Ser Val Asp Asp
206      130      135      140
209 Val Gly Ala Asp Tyr Glu Asp Tyr Thr Asp Met Leu Asn Lys Leu Asn
210 145      150      155      160
213 Asn Ala His Thr Gly Thr Thr Pro Thr Ser Glu Thr Thr Ala Glu Gly
214      165      170      175
217 Glu Gly Glu Thr Asp Ser Ala Ser Ser Ala Ser Asn Asp Asp Asn Val
218      180      185      190
221 Phe Asp Asp Phe Thr Ser Ser Asp Ala Leu Lys Lys Lys Gln Glu Arg
222      195      200      205

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225 Lys. Ser Arg Ser Ile Ala Asp Val Arg Asn Glu Glu Gln Asn Ile Gln
226      210      215      220
229 Gly Asn His Thr Glu Leu Gln Glu Lys Ser Ser Asn Glu Ala Ala Ser
230 225      230      235      240
233 Lys Glu Ser Pro Ala Ala Leu His Leu Arg Arg Arg Met His Ser Arg
234      245      250      255
237 His Arg His Leu Val Val Arg Lys Ala Arg Ser Glu Asp Ser Arg Pro
238      260      265      270
241 Ala Ala His Phe His Leu Ser Ser Arg Arg Arg His Gln Glu Ser Met
242      275      280      285
245 Gly Tyr His Gly Asp Met Tyr Ile Glu Asn Asp Arg Glu Arg Cys Ser
246      290      295      300
249 Tyr Gln Gly His Phe Gln Thr Arg Asp Gly Val Leu Thr Val Thr Asn
250 305      310      315      320
253 Ala Gly Leu Tyr Tyr Val Tyr Ala Gln Ile Trp Gly Tyr Asn Ser His
254      325      330      335
257 Asp Gln Asn Gly Phe Ile Val Phe Gln Gly Asp Thr Pro Phe Leu Gln
258      340      345      350
261 Cys Leu Asn Thr Val Pro Thr Asn Met Pro His Lys Val His Thr Cys
262      355      360      365
265 His Thr Ser Gly Leu Ile His Leu Glu Arg Asn Glu Arg Ile His Leu
266      370      375      380
269 Lys Asp Ile His Asn Asp Arg Asn Ala Val Leu Arg Glu Gly Asn Asn
270 385      390      395      400
273 Arg Ser Tyr Phe Gly Ile Phe Lys Val
274      405

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277 <210> SEQ ID NO: 3

278 <211> LENGTH: 1221

279 <212> TYPE: DNA

280 <213> ORGANISM: Drosophila melanogaster

282 <220> FEATURE:

283 <221> NAME/KEY: CDS

284 <222> LOCATION: (1)..(1218)

286 <400> SEQUENCE: 3

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289 1      5      10      15
291 gat gat ggt ttt ccg gcc aaa gcg acc agc acg gcg acc gcc cag cga      96
292 Asp Asp Gly Phe Pro Ala Lys Ala Thr Ser Thr Ala Thr Ala Gln Arg
293      20      25      30
295 cgc acc cgc cag ctg atc ccc ctg gtt ttg ggg ttc atc ggt ctg ggg      144
296 Arg Thr Arg Gln Leu Ile Pro Leu Val Leu Gly Phe Ile Gly Leu Gly
297      35      40      45
299 ctg gtc gtt gcc att ctc gca cta acg atc tgg cag aca acg cgt gta      192
300 Leu Val Val Ala Ile Leu Ala Leu Thr Ile Trp Gln Thr Thr Arg Val
301      50      55      60
303 tcg cat ctg gac aag gag ctg aag agc ctg aag cga gtc gtc gat aat      240
304 Ser His Leu Asp Lys Glu Leu Lys Ser Leu Lys Arg Val Val Asp Asn
305 65      70      75      80

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307 ctc cag cag cgt ttg ggc ata aac tat ctg gac gag ttc gac gag ttc      288
308 Leu Gln Gln Arg Leu Gly Ile Asn Tyr Leu Asp Glu Phe Asp Glu Phe
309      85      90      95
311 caa aag gag tac gag aat gcc ctc atc gac tat cca aaa aag gtg gat      336
312 Gln Lys Glu Tyr Glu Asn Ala Leu Ile Asp Tyr Pro Lys Lys Val Asp
313      100      105      110
315 ggc ctc acg gat gag gag gac gac gac gat ggc gat ggt ctg gat tcc      384
316 Gly Leu Thr Asp Glu Glu Asp Asp Asp Asp Gly Asp Gly Leu Asp Ser
317      115      120      125
319 att gcg gac gac gag gac gac gac gtt agc tat agc tct gtg gat gat      432
320 Ile Ala Asp Asp Glu Asp Asp Asp Val Ser Tyr Ser Ser Val Asp Asp
321      130      135      140
323 gtt ggc gca gac tac gag gac tac acc gat atg tta aat aaa ctc aac      480
324 Val Gly Ala Asp Tyr Glu Asp Tyr Thr Asp Met Leu Asn Lys Leu Asn
325 145      150      155      160
327 aat gca cat acc ggc acc acg ccc aca tct gag acc act gct gag ggc      528
328 Asn Ala His Thr Gly Thr Thr Pro Thr Ser Glu Thr Thr Ala Glu Gly
329      165      170      175
331 gag ggc gag acg gac agt gca tcc tca gcc tca aat gat gac aat gtg      576
332 Glu Gly Glu Thr Asp Ser Ala Ser Ser Ala Ser Asn Asp Asp Asn Val
333      180      185      190
335 ttc gat gac ttt acc agc tac aat gcc cac aaa aag aag cag gag aga      624
336 Phe Asp Asp Phe Thr Ser Tyr Asn Ala His Lys Lys Lys Gln Glu Arg
337      195      200      205
339 aaa tct cgc tcg att gcc gat gta cgc aat gag gag cag aat att caa      672
340 Lys Ser Arg Ser Ile Ala Asp Val Arg Asn Glu Glu Gln Asn Ile Gln
341      210      215      220
343 gga aat cac aca gag ctt cag gaa aag tca tcc aat gag gca act tcc      720
344 Gly Asn His Thr Glu Leu Gln Glu Lys Ser Ser Asn Glu Ala Thr Ser
345 225      230      235      240
347 aaa gag aga atg cat tcc cgc cat cgc cac ctc cta gtc cgc aaa ggt      768
348 Lys Glu Arg Met His Ser Arg His Arg His Leu Leu Val Arg Lys Gly
349      245      250      255
351 gaa tct ctt ctt tca gcc aga tcc gag gac tcg agg cca gca gcc cat      816
352 Glu Ser Leu Leu Ser Ala Arg Ser Glu Asp Ser Arg Pro Ala Ala His
353      260      265      270
355 ttc cac ttg agc agc agg cgg cgt cac caa gga agt atg ggc tac cat      864
356 Phe His Leu Ser Ser Arg Arg Arg His Gln Gly Ser Met Gly Tyr His
357      275      280      285
359 gga gat atg tac ata gga aat gat aac gag aga aac tct tat cag gga      912
360 Gly Asp Met Tyr Ile Gly Asn Asp Asn Glu Arg Asn Ser Tyr Gln Gly
361      290      295      300
363 cac ttt caa acg cgc gat ggc gtc ttg acg gtg acc aat aca ggc cta      960
364 His Phe Gln Thr Arg Asp Gly Val Leu Thr Val Thr Asn Thr Gly Leu
365 305      310      315      320
367 tat tac gta tac gcc cag ata tgc tac aac aac tcg cac gac cag aac      1008
368 Tyr Tyr Val Tyr Ala Gln Ile Cys Tyr Asn Asn Ser His Asp Gln Asn
369      325      330      335
371 gga ttt atc gtc ttt caa gga gac act cca ttc ctg cag tgc ttg aac      1056

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VERIFICATION SUMMARY

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Input Set : A:\PTO.txt

Output Set: N:\CRF3\04052001\I813329.raw

L:10 M:270 C: Current Application Number differs, Replaced Current Application No

L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date